

Serial Number: 09/924,840

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JUL 20 1995

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- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/424,840

DATE: 07/06/2000
TIME: 20:03:59

Input Set : A:\Pto.amc
Output Set: N:\CRF3\07062000\I424840.raw

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3 <110> APPLICANT: BERCHTOLD, Peter
4   ESCHER, Robert F.A.
6 <120> TITLE OF INVENTION: Anti-GPIIB/IIIA Recombinant Antibodies
8 <130> FILE REFERENCE: 100564-09049
10 <140> CURRENT APPLICATION NUMBER: US 09/424,840
11 <141> CURRENT FILING DATE: 1999-12-03
13 <150> PRIOR APPLICATION NUMBER: DE 19723904.8
14 <151> PRIOR FILING DATE: 1997-06-06
16 <150> PRIOR APPLICATION NUMBER: DE 19755227.7
17 <151> PRIOR FILING DATE: 1997-12-12
19 <150> PRIOR APPLICATION NUMBER: DE 19820663.1
20 <151> PRIOR FILING DATE: 1998-05-08
22 <160> NUMBER OF SEQ ID NOS: 127
24 <170> SOFTWARE: PatentIn Ver. 2.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 357
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
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32 <221> NAME/KEY: CDS
33 <222> LOCATION: (1)..(357)
35 <400> SEQUENCE: 1
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37  Gln  Val  Lys  Leu  Leu  Glu  Ser  Gly  Pro  Gly  Leu  Val  Lys  Pro  Ser  Glu
38      1              5              10              15
40  acc  ctg  tcc  ctc  aac  tgc  act  gtc  tct  ggt  cgc  tcc  atc  agt  ggt  tac      96
41  Thr  Leu  Ser  Leu  Asn  Cys  Thr  Val  Ser  Gly  Arg  Ser  Ile  Ser  Gly  Tyr
42      20              25              30
44  tct  tgg  aga  tgg  atc  cgg  cag  tct  cca  ggg  aag  gga  cta  gag  tgg  att      144
45  Ser  Trp  Arg  Trp  Ile  Arg  Gln  Ser  Pro  Gly  Lys  Gly  Leu  Glu  Trp  Ile
46      35              40              45
48  ggg  gat  atc  tct  tat  agt  ggg  agt  acc  aag  tac  aaa  ccc  tcc  ctc  agg      192
49  Gly  Asp  Ile  Ser  Tyr  Ser  Gly  Ser  Thr  Lys  Tyr  Lys  Pro  Ser  Leu  Arg
50      50              55              60
53  agt  cga  gtc  acc  ctg  tca  gta  gac  acg  tcc  aag  aac  cag  ttc  tcc  ctg      240
54  Ser  Arg  Val  Thr  Leu  Ser  Val  Asp  Thr  Ser  Lys  Asn  Gln  Phe  Ser  Leu
55      65              70              75              80
57  aag  ctg  aat  tcg  gtg  acc  gct  gcg  gac  acg  gcc  gtc  tat  tac  tgt  gcg      288
58  Lys  Leu  Asn  Ser  Val  Thr  Ala  Ala  Asp  Thr  Ala  Val  Tyr  Tyr  Cys  Ala
59      85              90              95
61  cga  gtc  ttg  ccc  ttt  gac  ccg  atc  tcg  atg  gac  gtc  tgg  ggc  aaa  ggg      336
62  Arg  Val  Leu  Pro  Phe  Asp  Pro  Ile  Ser  Met  Asp  Val  Trp  Gly  Lys  Gly
63      100              105              110
65  acc  acg  gtc  acc  gtc  tcc  tca
66  Thr  Thr  Val  Thr  Val  Ser  Ser
67      115
70 <210> SEQ ID NO: 2

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71 <211> LENGTH: 119
72 <212> TYPE: PRT
73 <213> ORGANISM: Homo sapiens
75 <400> SEQUENCE: 2
76 Gln Val Lys Leu Leu Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
77   1           5           10           15
79 Thr Leu Ser Leu Asn Cys Thr Val Ser Gly Arg Ser Ile Ser Gly Tyr
80           20           25           30
82 Ser Trp Arg Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
83           35           40           45
85 Gly Asp Ile Ser Tyr Ser Gly Ser Thr Lys Tyr Lys Pro Ser Leu Arg
86           50           55           60
88 Ser Arg Val Thr Leu Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
89           65           70           75           80
91 Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
92           85           90           95
94 Arg Val Leu Pro Phe Asp Pro Ile Ser Met Asp Val Trp Gly Lys Gly
95           100          105          110
97 Thr Thr Val Thr Val Ser Ser
98           115
102 <210> SEQ ID NO: 3
103 <211> LENGTH: 333
105 <212> TYPE: DNA
106 <213> ORGANISM: Homo sapiens
108 <220> FEATURE:
109 <221> NAME/KEY: CDS
110 <222> LOCATION: (1)..(333)
112 <400> SEQUENCE: 3
113 gtg gtg act cag cca ccc tca gcg tct ggg acc ccc ggg cag tgg gtc 48
114 Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Trp Val
115   1           5           10           15
117 acc atc tct tgt tct ggg agc agc tcc aac atc aga agt aat cct gtt 96
118 Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Arg Ser Asn Pro Val
119           20           25           30
121 agc tgg tat cac cag gtc cca ggc acg gcc ccc aaa ctc ctc atc ttt 144
122 Ser Trp Tyr His Gln Val Pro Gly Thr Ala Pro Lys Leu Leu Ile Phe
123           35           40           45
125 ggt agt cat cag cgg ccc tca ggg gtc cct gac cga ttc tct ggc tcc 192
126 Gly Ser His Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
127           50           55           60
129 aag tcg ggc acc tcc gcc tcc ctg gcc atc cgt ggg ctc caa tct ggg 240
130 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Arg Gly Leu Gln Ser Gly
131           65           70           75           80
133 gat gct ggt gac tat tac tgt gca aca tgg gat gac ggc ctc aat ggt 288
134 Asp Ala Gly Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Gly Leu Asn Gly
135           85           90           95
137 ccg gtg ttc ggc gga ggg acc aag ctg acc gtc cta agt cag ccc 333
138 Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro
139           100          105          110

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143 <211> LENGTH: 111
144 <212> TYPE: PRT
145 <213> ORGANISM: Homo sapiens
147 <400> SEQUENCE: 4
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149 1 5 10 15
151 Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Arg Ser Asn Pro Val
152 20 25 30
154 Ser Trp Tyr His Gln Val Pro Gly Thr Ala Pro Lys Leu Ile Phe
155 35 40 45
157 Gly Ser His Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
158 50 55 60
160 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Arg Gly Leu Gln Ser Gly
161 65 70 75 80
163 Asp Ala Gly Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Gly Leu Asn Gly
164 85 90 95
166 Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro
167 100 105 110

171 <210> SEQ ID NO: 5
172 <211> LENGTH: 369
173 <212> TYPE: DNA
174 <213> ORGANISM: Homo sapiens
176 <220> FEATURE:
177 <221> NAME/KEY: CDS
178 <222> LOCATION: (1)..(369)
180 <400> SEQUENCE: 5
181 cag gtg aaa ctg ctg gag tct ggg gga ggc gtg gtc cag cct ggg agg 48
182 Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Arg
183 1 5 10 15
185 tcc ctg aga ctg tcc tgt gca gcc tct gga ttc acc ttc agt agc tat 96
186 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
187 20 25 30
189 gct atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
190 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
191 35 40 45
193 gca gtt ata tca tat gat gga agc aat aaa tac tac gca gac tcc gtg 192
194 Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
195 50 55 60
197 aag ggc cga ttc gcc atc tcc aga gac aat tcc aag aac acg ctg tat 240
198 Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
199 65 70 75 80
201 ctg caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac tgt 288
202 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
203 85 90 95
205 gcg aga gcg ctg ggg agc tgg ggg ggt tgg gac cac tac atg gac gtc 336
206 Ala Arg Ala Leu Gly Ser Trp Gly Gly Trp Asp His Tyr Met Asp Val
207 100 105 110
209 tgg ggc aaa ggg acc acg gtc acc gtc tcc tca 369

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215 <211> LENGTH: 123
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217 <213> ORGANISM: Homo sapiens
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221      1      5      10      15
223 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
224      20      25      30
226 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
227      35      40      45
229 Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
230      50      55      60
232 Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
233      65      70      75      80
235 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
236      85      90      95
238 Ala Arg Ala Leu Gly Ser Trp Gly Gly Trp Asp His Tyr Met Asp Val
239      100     105     110
241 Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
242      115                      120
246 <210> SEQ ID NO: 7
247 <211> LENGTH: 333
248 <212> TYPE: DNA
249 <213> ORGANISM: Homo sapiens
251 <220> FEATURE:
252 <221> NAME/KEY: CDS
253 <222> LOCATION: (1)..(333)
255 <400> SEQUENCE: 7
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258      1      5      10      15
261 acc atc tct tgt tct gga agc agc tcc aac atc gga agt aat act gta      96
262 Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Thr Val
263      20      25      30
265 aac tgg tac cag cag ctc cca gga acg gcc ccc aaa ctc ctc atc tat      144
266 Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr
267      35      40      45
269 agt aat aat cag cgg ccc tca ggg gtc cct gac cga ttc tct ggc tcc      192
270 Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
271      50      55      60
273 aag tct ggc acc tca gcc tcc ctg gcc atc agt ggg ctc cag tct gag      240
274 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu
275      65      70      75      80
277 gat gag gct gat tat tac tgt gca gca tgg gat gac agc ctg aat ggt      288
278 Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu Asn Gly
279      85      90      95

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281 tgg gtg ttc ggc gga ggg acc aag ctg acc gtc cta ggt cag ccc      333
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283      100                      105                      110
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287 <211> LENGTH: 111
288 <212> TYPE: PRT
289 <213> ORGANISM: Homo sapiens
291 <400> SEQUENCE: 8
292 Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val
293      1                      5                      10                      15
295 Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Thr Val
296      20                      25                      30
298 Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr
299      35                      40                      45
301 Ser Asn Asn Gln Arg Pro Ser Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
302      50                      55                      60
304 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu
305      65                      70                      75                      80
307 Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu Asn Gly
308      85                      90                      95
310 Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
311      100                      105                      110
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316 <211> LENGTH: 369
317 <212> TYPE: DNA
318 <213> ORGANISM: Homo sapiens
320 <220> FEATURE:
321 <221> NAME/KEY: CDS
322 <222> LOCATION: (1)..(369)
324 <400> SEQUENCE: 9
325 cag gtg aaa ctg ctc gag tct ggg gga ggc ttg gtt cac ccc ggg ggg      48
326 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val His Pro Gly Gly
327      1                      5                      10                      15
329 tcc ctg aga ctc tct tgt gca gcc tct gga ttt acg ttt gac aac ttt      96
330 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Phe
331      20                      25                      30
333 gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtc      144
334 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
335      35                      40                      45
337 tca ggc att agt ggt ggt ggt ctt ttg aca cac tac gca gac tcc gtg      192
338 Ser Gly Ile Ser Gly Gly Gly Leu Leu Thr His Tyr Ala Asp Ser Val
339      50                      55                      60
341 aag ggc cgg ttc acc atc tcc aga aac aat tcc agg aac act gta tac      240
342 Lys Gly Arg Phe Thr Ile Ser Arg Asn Asn Ser Arg Asn Thr Val Tyr
343      65                      70                      75                      80
345 cta caa atg aac agc ctg aga gcc gaa gac acg gcc gtg tat tat tgt      288
346 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
347      85                      90                      95
349 gtg aga gat ctg ggc tat aga gta ctt tcg act ttt act ttt gat atc      336

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